



Speciation over 200 million years – What makes an *Aspergillus* species

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POSTER SESSION ABSTRACTS
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CS5T46

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Speciation over 200 million years – What makes an *Aspergillus* species.

The study of speciation, how new species arise, diverge and remain separate, has a central role in evolutionary biology. Partly because it embraces so many disciplines, including population genetics, behavioral sciences, comparative genomics, evolutionary biology, biodiversity, biogeography and ecology. It also remains one of the most fascinating questions in evolution. We try to answer the questions surrounding speciation in the filamentous fungi *Aspergillus* because of the diversity of the genus. It holds species relevant to plant and human pathology, food biotechnology, enzyme production, model organisms, and even includes some extremophiles. Speciation is nearly impossible to study and in most cases, we know very little about the genetic basis of species formation. But in this project we look at approximately 300 newly sequenced *Aspergilli* across an evolutionary span of 200 million years. This is, in evolutionary terms, a high number of species per million years, which allows us to approach the genes and functions that defines the *Aspergillus* genus and its pan, core, section and clade genomes. But we also aim to identify the genes that are involved in speciation and those unique to the individual species. To identify potential evolutionary events, we group the *Aspergillus* genomes into functional similar families (homologs), by using a novel homologous grouping method based on protein sequence similarity and functional domain prediction that maps the homologous families' genotypes to phenotypes. From this we can highlight previously unknown incidents that can affect speciation, such as horizontal gene transfers between closely or distantly related species, chromosomal rearrangements, gene duplications, creations and losses and propose genome-founded hypotheses on which types of genes drive speciation in *Aspergillus*.

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